

CLAIMS

1. A method of associative analysis, comprising:
 - collecting a plurality of expression profiles of a control group and a plurality of expression profiles of an experimental group;
 - normalizing the plurality of expression profiles of the control group relative to their backgrounds;
 - normalizing the plurality of expression profiles of the experimental group relative to their backgrounds;
 - adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to identify outliers and to re-scale to an averaged profile of the control group;
 - identifying a group of similarly expressed genes, defining a reference group, determined from the plurality of expression profiles of the control group;
 - identifying a plurality of differentially expressed genes in the plurality of expression profiles of the experimental group based on the reference group, wherein identifying the plurality of differentially expressed genes comprises utilizing a paired T-test and an associative T-test; and
 - classifying the differentially expressed genes as (a) likely false positive, (b) real positives, or (c) potential positives using the paired T-test and associate T-test.
2. The method of claim 1, wherein identifying the plurality of differentially expressed genes further comprises utilizing a Bonferroni T-test.

3. The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group comprises:

selecting a plurality of genes from the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group, wherein the plurality of genes are expressed above a background; and

scaling the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to an average profile of the plurality of expression profiles of the control group.

4. The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group comprises analyzing by regression analysis the plurality of genes expressed above the background.

5. The method of claim 1, wherein adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group comprises selecting equally expressed genes as a homogenous family of genes with normally distributed residuals measured as deviations from a regression line that is calculated against an average profile.

6. The method of claim 1, wherein the reference group comprises a group of genes expressed above background levels with normal low variability of expression in control samples as determined by a F-test.

7. The method of claim 1, wherein the reference group has residuals that approximate a normal distribution, based on a Kolmogorov-Smirnov criterion.
8. The method of claim 1, wherein the associative T-test comprises a test in which a plurality of replicated residuals for each gene of the plurality of the expression profiles of the experimental group are compared with an entire set of residuals from the plurality of expression profiles of the control group.
9. The method of claim 1, wherein the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group comprise an array.
10. The method of claim 1, wherein classifying comprises:
 - classifying the genes identified as expressed by the paired T-test as false positive;
 - classifying the genes identified as expressed by the paired T-test and the associative T-test as real positives; and
 - classifying the genes identified as expressed by the associative T-test as potentially real positives.
11. The method of claim 10, wherein the genes identified as expressed by the associative T-test are tested again.

12. The method of claim 1, wherein identifying a group of similarly expressed genes determined from the plurality of expression profiles of the control group further comprises excluding outliers from the plurality of expression profiles of the control group.

13. A method of associative analysis, comprising:

collecting a plurality of expression profiles of a control group and a plurality of expression profiles of an experimental group;

normalizing the plurality of expression profiles of the control group relative to their backgrounds;

normalizing the plurality of expression profiles of the experimental group relative to their backgrounds;

adjusting the plurality of expression profiles of the control group and the plurality of expression profiles of the experimental group to identify outliers and to re-scale to an averaged profile of the control group;

identifying a group of similarly expressed genes, defining a reference group, determined from the plurality of expression profiles of the control group, the reference group comprising a group of genes expressed above background levels with normal low variability of expression in control samples as determined by a F-test;

identifying a plurality of differentially expressed genes in the plurality of expression profiles of the experimental group based on the reference group, wherein identifying the plurality of differentially expressed genes comprises utilizing a paired T-test, a Bonferroni T-test, and an associative T-test;

classifying the genes identified as expressed by the paired T-test as false positive;
classifying the genes identified as expressed by the paired T-test and the associative T-test
as real positives; and
classifying the genes identified as expressed by the associative T-test as potentially real
positives.